



Rev. 10/93

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN THE APPLICATION OF:
STEPHEN M. ALLEN

CASE NO.: BB1429 US NA

APPLICATION NO.: 09/740,288

GROUP ART UNIT: UNKNOWN

FILED: CONCURRENTLY HERewith

EXAMINER: UNKNOWN

FOR: PLANT BIOTIN SYNTHASE

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

DECLARATION IN ACCORDANCE WITH 37 CFR 1.821

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively are the same.

Respectfully submitted,

KENING LI
ATTORNEY FOR A

KENING LI
ATTORNEY FOR APPLICANTS
REGISTRATION NO. 44,872
TELEPHONE: 302-992-3749
FACSIMILE: 302-892-1026

Dated: 04/10/2001

[illegible]



#5

SEQUENCE LISTING

<110> Allen, Stephen
Kinney, Anthony
Miao, Guo-Hua
Orozco, Emil

<120> PLANT BIOTIN SYNTHASE

<130> BB1429 US NA

<140> US 09/740288

<141> 2000-12-19

<150> US 60/172929

<151> 1999-12-21

<160> 36

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<213> Hordeum vulgare

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 35 40 45
 Thr Arg Pro Glu Ile Gln Ala Ile Tyr Asp Ser Pro Leu Leu Asp Leu
 50 55 60
 Leu Phe His Gly Ala Gln Val His Arg Asn Val His Lys Phe Arg Glu
 65 70 75 80
 Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu
 85 90 95
 Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Leu Lys
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 Arg Ala Ile Arg Asp Gly Pro Arg Asn Asp Trp Ser Arg Pro Glu Xaa
 35 40 45
 Xaa Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Xaa
 50 55 60

Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Gly Gln Lys Leu Met Asn
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tatcatggcc ttgatgctgc tagcgcgcaa cctgcgctcc cgcctccgcc caccgctcgc 180
cgccgccgcg gngttctcgt cggcccgcggc ggaggcgag agggcgatac gggacgggcc 240
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cctctttcac ggggctcaag tccacagaaa tgtccataaa ttcaagagaa gtgcagcaat 360
gcacacttct ttcaatcaag actggtggga tgcagtgaag attgttctta ctgtcctcaa 420
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 35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
 50 55 60
 Gln Val His Arg Asn Val His Xaa Ser Arg Glu Val Gln Gln Cys Thr
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 aaaaaaggca aaagagtctg ggagcaccog tttttgcatg ggagctgcat ggagagaaac 540
 cattggcagg aaatcaaact tcaaccagat tcttgaatat gtcaaggaaa taaggggtat 600
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35 40 45
Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
50 55 60
Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
65 70 75 80
Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
85 90 95
Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
100 105 110
Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
115 120 125
Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
130 135 140
Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
145 150 155 160
Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln
165 170 175
Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
180 185 190
Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr
195 200 205
Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser
210 215 220
Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
225 230 235 240
Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
245 250 255
Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp
260 265 270
Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala
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Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
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 gagagctcgt cttcgacctt tgatttttcat ttctacattt tcttctctct catcatcttc 180
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 tgacactgga gtgaaagccc aaaagctgat gaacaaggga cgcagttctg caaggaagca 480
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 tacaatgggg aangaagaac aa 562

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 <212> PRT
 <213> Argemone mexicana

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 Ala Val Gln Ala Glu Arg Thr Ile Lys Glu Gly Pro Arg Asn Asp Trp
 35 40 45
 Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu
 50 55 60
 Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu
 65 70 75 80
 Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu
 85 90 95
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 35 40 45
 Val Lys Ser Ile Tyr Asp Ser Pro Ile Leu Asp Leu Leu Phe His Gly
 50 55 60
 Ala Gln Val His Arg His Ala His Asn Phe Arg Glu Val Gln Gln Cys
 65 70 75 80
 Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr
 85 90 95
 Cys Pro Gln Ser Ser Lys Tyr Asp Thr Gly Val Lys Arg Pro Ser Leu
 100 105 110
 Met Asn Lys Glu Ala Val Leu Gln Ala Ala Lys Lys Ala Lys Glu Ala
 115 120 125
 Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Thr Leu Gly
 130 135 140
 Arg Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg
 145 150 155 160

Asp Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln
 165 170 175
 Gln Ala Val Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn
 180 185 190
 Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Thr
 195 200 205
 Tyr Asp Glu Arg Leu Gln Thr Leu Glu Phe Val Arg Asp Ala Gly Ile
 210 215 220
 Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp
 225 230 235 240
 Arg Val Gly Leu Leu His Thr Leu Ser Thr Leu Pro Thr His Pro Glu
 245 250 255
 Ser Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu
 260 265 270
 Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr
 275 280 285
 Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg
 290 295 300
 Val Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala
 305 310 315 320
 Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr Pro Asn Asn Asp
 325 330 335
 Phe Asp Ala Asp Gln Leu Met Phe Lys Val Leu Gly Leu Leu Pro Lys
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 <211> 52
 <212> PRT
 <213> Glycine max

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 20 25 30

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Gly	Cys	Ser	Glu												
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tgtcaaggac ataagaggta tgggcatgga ggtctgttgc accctgggca tgctagagaa 180
acaacaagct gaagaactcc aagaaggctg gactttacag cttataatca taacctaaaga 240
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tagatttacc agtcctttc nagcatgtcc cnttnnaagc tgggaattaa gccgtcctgg 360
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<211> 78

<212> PRT

<213> Triticum aestivum

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Glu Leu Gln Glu Xaa Asp Phe Thr Ala Tyr Asn His Asn Leu
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aggcggagcg	ggcgggtgcg	gacggggcca	ggaacgacgt	gaccgcggcc	gagatccagg			240
ccatctacga	ctccccgctc	ctcgacctcc	tcttccacgg	ggctcaagtc	cataggaatg			300
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<212>	PRT
<213>	Hordeum vulgare

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			20					25					30				
Ser	Leu	Arg	Ser	Arg	Val	Arg	Ser	Pro	Phe	Ala	Ser	Ala	Val	Ser	Ala		
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Ala	Pro	Phe	Ser	Ser	Val	Ser	Ala	Ala	Ala	Ala	Glu	Ala	Glu	Arg	Ala		
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65					70					75					80		
Ile	Tyr	Asp	Ser	Pro	Leu	Leu	Asp	Leu	Leu	Phe	His	Gly	Ala	Gln	Val		
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His	Arg	Asn	Val	His	Lys	Phe	Arg	Glu	Val	Gln	Gln	Cys	Thr	Leu	Leu		
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Ser	Ile	Lys	Thr	Gly	Gly	Cys	Ser	Glu	Asp	Cys	Ser	Tyr	Cys	Pro	Gln		
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 Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr
 145 150 155 160
 Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg Lys Thr
 165 170 175
 Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly Met Gly
 180 185 190
 Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Glu
 195 200 205
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 210 215 220
 Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr Asp Asp
 225 230 235 240
 Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser Val Cys
 245 250 255
 Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly
 260 265 270
 Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser Val Pro
 275 280 285
 Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp Gln Lys
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 Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg Phe
 325 330 335
 Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile
 340 345 350
 Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe Asp Ala
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 Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala Pro Asn
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 <213> Zea mays

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 cgactggagc cggccccgaga tccaggccgt ctacgactca ccgctcctcg acctcctctt 360
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275 280 285
 Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe Asp
 290 295 300
 Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala Pro
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 Ser Phe Gly Glu Glu Glu Ala Ser Ala Ala Pro Thr Glu Ser Glu
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 Arg Ser Glu Gln Ala Ala Ser Met
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 <211> 1515
 <212> DNA
 <213> Zea mays

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 gcaatgcaca cttctttcaa tcaagactgg tggatgcagt gaagattgtt cttactgtcc 420
 tcagtcatca agatacaaca ctggattgaa ggcccaaaaa ttgatgaaca aagatgctgt 480
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<210> 22
 <211> 377
 <212> PRT
 <213> Zea mays

<400> 22
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35 40 45
 Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
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 Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
 65 70 75 80
 Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
 85 90 95
 Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
 100 105 110
 Asn Lys Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
 115 120 125
 Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
 130 135 140
 Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
 145 150 155 160
 Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln
 165 170 175
 Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
 180 185 190
 Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr
 195 200 205
 Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser
 210 215 220
 Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
 225 230 235 240
 Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
 245 250 255
 Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp
 260 265 270
 Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala
 275 280 285
 Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
 290 295 300
 Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
 305 310 315 320
 Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
 325 330 335
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 340 345 350
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 355 360 365
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 <212> DNA
 <213> Zea mays

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 gcgttctcgt cggccgcggc ggaggcggag agggcgatac gggacgggcc gcggaacgac 240
 tggagccggc ccgagatcca ggccgtctac gactcacccg tcctcgacct cctctttcac 300

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<210> 24
 <211> 377
 <212> PRT
 <213> Zea mays

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<400> 24
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35 40 45
Gln Ala Val Tyr Asp Ser Pro Leu Leu Asp Leu Leu Phe His Gly Ala
50 55 60
Gln Val His Arg Asn Val His Lys Phe Arg Glu Val Gln Gln Cys Thr
65 70 75 80
Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
85 90 95
Pro Gln Ser Ser Arg Tyr Asn Thr Gly Leu Lys Ala Gln Lys Leu Met
100 105 110
Asn Lys Tyr Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ser Gly
115 120 125
Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
130 135 140
Lys Ser Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Glu Ile Arg Gly
145 150 155 160
Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Ile Glu Lys Gln Gln
165 170 175
Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
180 185 190
Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Thr Thr Arg Ser Tyr
195 200 205
Asp Asp Arg Leu Gln Thr Leu Glu His Val Arg Glu Ala Gly Ile Ser
210 215 220
Ile Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg

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225		230		235		240
Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser						
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Val Pro Ile Asn Ala Leu Val Ala Val Lys Gly Thr Pro Leu Glu Asp						
		260		265		270
Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Thr Ala						
		275		280		285
Arg Ile Thr Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val						
		290		295		300
Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn						
		305		310		315
Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe						
		325		330		335
Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala						
		340		345		350
Pro Ser Phe Gly Glu Glu Glu Ala Ser Ala Ala Ala Pro Thr Glu Ser						
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Glu Arg Ser Glu Gln Ala Ala Ser Met						
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<210> 25
 <211> 1477
 <212> DNA
 <213> Argemone mexicana

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<210> 26
 <211> 379

<212> PRT
 <213> Argemone mexicana

<400> 26

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35      40      45
Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Val Leu Asp Leu
50      55      60
Leu Phe His Ala Ala Gln Val His Arg His Ala His Asn Phe Arg Glu
65      70      75      80
Val Gln Gln Cys Thr Leu Leu Ser Val Lys Thr Gly Gly Cys Ser Glu
85      90      95
Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Asp Thr Gly Val Lys
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Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg
130     135     140
Asp Thr Val Gly Arg Lys Thr Asn Phe Lys Gln Ile Leu Glu Tyr Val
145     150     155     160
Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met
165     170     175
Ile Glu Lys Gln Gln Ala Val Glu Leu Lys Gln Ala Gly Leu Thr Ala
180     185     190
Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile
195     200     205
Thr Thr Arg Ser Tyr Asp Glu Arg Leu Glu Thr Leu Gln Phe Val Arg
210     215     220
Glu Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu
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Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro
245     250     255
Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly
260     265     270
Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg
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Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu
290     295     300
Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe
305     310     315     320
Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr
325     330     335
Pro Asn Asn Asp Phe Asp Ala Asp Gln Met Met Phe Lys Ile Leu Gly
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Leu Thr Pro Lys Ala Pro Asn Phe Asp Gln Thr Ser Thr Ser Phe Glu
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<210> 27
 <211> 1526



<212> DNA
<213> Glycine max

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tataaggaag cagcttcttc tagttgagtt gtcaacggtt tcaaaacaat atctgtgatc 1380
cttcaacttc tctaattgct cattagcatg tactgatgtt aggtttcatt gaatttgtct 1440
aatctcagct ttgaagacac aaactccaac acttaaaaat aaatattgaa attattgatt 1500
tttccctaaa aaaaaaaaaa aaaaaa 1526

<210> 28
<211> 415
<212> PRT
<213> Glycine max

<400> 28
Thr Lys Pro Asn Pro Lys His Lys Tyr Arg Cys Cys Leu Leu Ser Leu
1 5 10 15
Ser Cys Leu Tyr Ser Gln Ile Ser His Ser Phe Ser Val Val Ser Leu
20 25 30
Pro Asn Phe Glu Phe Glu Ser Lys Asn Met Phe Leu Ala Arg Pro Ile
35 40 45
Phe Arg Ala Pro Ser Leu Trp Ala Leu His Ser Ser Tyr Ala Tyr Ser
50 55 60
Ser Ala Ser Ala Ala Ala Ile Gln Ala Glu Arg Ala Ile Lys Glu Gly
65 70 75 80
Pro Arg Asn Asp Trp Ser Arg Asp Gln Val Lys Ser Ile Tyr Asp Ser
85 90 95
Pro Ile Leu Asp Leu Leu Phe His Gly Ala Gln Val His Arg His Ala
100 105 110
His Asn Phe Arg Glu Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr
115 120 125
Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys Pro Gln Ser Ser Lys Tyr
130 135 140

Asp Thr Gly Val Lys Gly Gln Arg Leu Met Asn Lys Glu Ala Val Leu
 145 150 155 160
 Gln Ala Ala Lys Lys Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met
 165 170 175
 Gly Ala Ala Trp Arg Asp Thr Leu Gly Arg Lys Thr Asn Phe Asn Gln
 180 185 190
 Ile Leu Glu Tyr Val Lys Asp Ile Arg Asp Met Gly Met Glu Val Cys
 195 200 205
 Cys Thr Leu Gly Met Leu Glu Lys Gln Gln Ala Val Glu Leu Lys Lys
 210 215 220
 Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr
 225 230 235 240
 Tyr Pro Asn Ile Ile Thr Thr Arg Thr Tyr Asp Glu Arg Leu Gln Thr
 245 250 255
 Leu Glu Phe Val Arg Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile
 260 265 270
 Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg Val Gly Leu Leu His Thr
 275 280 285
 Leu Ser Thr Leu Pro Thr His Pro Glu Ser Val Pro Ile Asn Ala Leu
 290 295 300
 Val Ala Val Lys Gly Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile
 305 310 315 320
 Trp Glu Met Ile Arg Met Ile Ala Thr Ala Arg Ile Val Met Pro Lys
 325 330 335
 Ala Met Val Arg Leu Ser Ala Gly Arg Val Arg Phe Ser Met Pro Glu
 340 345 350
 Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu
 355 360 365
 Lys Leu Leu Thr Thr Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met
 370 375 380
 Phe Lys Val Leu Gly Leu Leu Pro Lys Ala Pro Ser Leu His Glu Gly
 385 390 395 400
 Glu Thr Ser Val Thr Glu Asp Tyr Lys Glu Ala Ala Ser Ser Ser
 405 410 415

<210> 29
 <211> 1659
 <212> DNA
 <213> Glycine max

<400> 29
 aaagagtgtg tacagataga tttccaaact ccaactcactc accactatgg cgactctcag 60
 aacttcctta tcacgatccc tcatcctcct tcgctccaat acccctaaac tcgcacctat 120
 ctcttctctt gttcgtcttc aagttcaaaa gtcgagaaac tatgggtaccg tatcatctgt 180
 tcctcctcaa gctacagaaa catcaagcac atcacctagt aaggatgtct accaagaagc 240
 actcaacgca actgaacccc gcagcaattg gacaagagaa gaaatcaagg cgatctatga 300
 taagccattg atggagtatt gttgggggtgc tggtagtttg cacaggaaat tccatatacc 360
 tggggctatt cagatgtgta cattgttgaa catcaagacg ggtgggttgct cggaggattg 420
 ttcttactgc gcccaatcat ccgctacca aaccggtctc aaagcctcca aaatggtctc 480
 cgtcgaatct gtcctcgcag ccgcccgcac cgccaaagac aacggtagta cacgtttctg 540
 catgggagcc gcgtggcgcg atatgcgtgg acgaaaaacc aatctcaaaa atgtcaaaac 600
 aatggtttagc gagattcgcg gaatgggtat ggaagtatgt gtcacgcttg gtatgattga 660
 tgcagagcaa gtcaggaac tcaaagaagc cgggtctcagc gcttataatc ataatgtgga 720
 tacgtcgagg gatttctatc ccaaggttat cacgaccagg acttatgatg agagattgga 780
 taccattaag aatgtgagag aggccggaat caatgtttgt acgggtggaa tcctcggatt 840

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aggagaaaaat aagtctgacc atattggact tttggagacg gttgctacgt tgccttcgca 900
tccggaatca tttcctgtga acatgttagt ggctatcaaa ggaacaccac tggaaggaaa 960
caagaagggtg gaatttgaga atatgttgag aatggttgcg acggctagaa tcgtcatgcc 1020
taaaaccatc gtgcgttttg cagctggaag aggagaattg agcgaggaac aacaggtctt 1080
atgtttcatg gccggagcca atgocgtttt cacaggagaa acaatgtaa ccacaccagc 1140
cgttggatgg ggtgtcgatt ccgtcgtttt caacagatgg ggattaagac ccatggaaaag 1200
tttcgaggtt gaagccttga agaacgataa acctgccact actaatacgg aaataccggt 1260
agaggcaagt aaggcagaga tgccaggtag agttgcttga ttgattgttt gatttggata 1320
cccagggcgt ttggtgcgct catcatctcg agtttttgca aggagattcg aacagtggaa 1380
gtgccgttgc gccaccattg ggattggcgt atcggactga gattgactgt gccacgaaaa 1440
tgttttgcgc tatcgtgtgt tgtcatctcg tgggaattta gcgttgtttg ttttgttttt 1500
ggttttgttt gatgtgagag aatgattgtt tagaagggga gaatgtatat acggaacagt 1560
agaatatatt cttgtctata agattatata ggataaatat atataagctt atcctcaaaa 1620
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1659

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<210> 30
<211> 417
<212> PRT
<213> Glycine max

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<400> 30
Met Ala Thr Leu Arg Thr Ser Leu Ser Arg Ser Leu Ile Leu Leu Arg
1      5      10      15
Ser Asn Thr Pro Lys Leu Ala Pro Ile Ser Ser Ser Val Arg Leu Gln
20     25     30
Val Gln Lys Ser Arg Asn Tyr Gly Thr Val Ser Ser Val Pro Pro Gln
35     40     45
Ala Thr Glu Thr Ser Ser Thr Ser Pro Ser Lys Asp Val Tyr Gln Glu
50     55     60
Ala Leu Asn Ala Thr Glu Pro Arg Ser Asn Trp Thr Arg Glu Glu Ile
65     70     75
Lys Ala Ile Tyr Asp Lys Pro Leu Met Glu Leu Cys Trp Gly Ala Gly
85     90     95
Ser Leu His Arg Lys Phe His Ile Pro Gly Ala Ile Gln Met Cys Thr
100    105    110
Leu Leu Asn Ile Lys Thr Gly Gly Cys Ser Glu Asp Cys Ser Tyr Cys
115    120    125
Ala Gln Ser Ser Arg Tyr Gln Thr Gly Leu Lys Ala Ser Lys Met Val
130    135    140
Ser Val Glu Ser Val Leu Ala Ala Ala Arg Ile Ala Lys Asp Asn Gly
145    150    155    160
Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Asp Met Arg Gly Arg
165    170    175
Lys Thr Asn Leu Lys Asn Val Lys Thr Met Val Ser Glu Ile Arg Gly
180    185    190
Met Gly Met Glu Val Cys Val Thr Leu Gly Met Ile Asp Ala Glu Gln
195    200    205
Ala Gln Glu Leu Lys Glu Ala Gly Leu Thr Ala Tyr Asn His Asn Val
210    215    220
Asp Thr Ser Arg Asp Phe Tyr Pro Lys Val Ile Thr Thr Arg Thr Tyr
225    230    235    240
Asp Glu Arg Leu Asp Thr Ile Lys Asn Val Arg Glu Ala Gly Ile Asn
245    250    255
Val Cys Thr Gly Gly Ile Leu Gly Leu Gly Glu Asn Lys Ser Asp His
260    265    270

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Ile Gly Leu Leu Glu Thr Val Ala Thr Leu Pro Ser His Pro Glu Ser
275 280 285
Phe Pro Val Asn Met Leu Val Ala Ile Lys Gly Thr Pro Leu Glu Gly
290 295 300
Asn Lys Lys Val Glu Phe Glu Asn Met Leu Arg Met Val Ala Thr Ala
305 310 315 320
Arg Ile Val Met Pro Lys Thr Ile Val Arg Leu Ala Ala Gly Arg Gly
325 330 335
Glu Leu Ser Glu Glu Gln Gln Val Leu Cys Phe Met Ala Gly Ala Asn
340 345 350
Ala Val Phe Thr Gly Glu Thr Met Leu Thr Thr Pro Ala Val Gly Trp
355 360 365
Gly Val Asp Ser Val Val Phe Asn Arg Trp Gly Leu Arg Pro Met Glu
370 375 380
Ser Phe Glu Val Glu Ala Leu Lys Asn Asp Lys Pro Ala Thr Thr Asn
385 390 395 400
Thr Glu Ile Pro Val Glu Ala Ser Lys Ala Glu Met Pro Gly Thr Val
405 410 415
Ala

<210> 31
<211> 1032
<212> DNA
<213> Triticum aestivum

<400> 31
gcacgagaga tgccgtccta gaagcagcaa aaaaggcaaa ggaggctggg agcaccgat 60
tttgcattggg agccgcatgg agagagacaa ttggcaggaa aacaaatttc aaccagattc 120
ttgaatatgt caaggacata agaggtatgg gcatggaggt ctgttgacc ctgggcatgc 180
tagagaaaca acaagctgaa gaactcaaga aggctggact tacagcttat aatcataacc 240
tagatacatc aagagaatat taccccaaca ttatttctac aagatcgtag gatgatagat 300
tacagactct tcagcatgtc cgtgaagctg gaataagcgt ctgctcaggt ggaattattg 360
gtcttggaag ggcggaggaa gaccgtgtag ggctgttgca tacactggcc actttgccaa 420
cacaccaga gagcgcttct atcaatgcat tgattgctgt caaaggcacg cctcttcagg 480
atcagaagcc tgtagagata tgggaaatga tccgcatgat tgccagcgca cggattgtga 540
tgccaaaggc aatggtgaga ctttcggcag ggagagtacg gttttccatg ccagaacaag 600
ctctctgctt tctcgctggg gccaaactoga tcttcgccgg tgaaaagctc ctgacaactg 660
cgaacaatga ctttgatgcg gaccaggcaa tgttcaagat ccttggcctg attcccaagg 720
ctccaaactt tggcgatgaa gaggtcatgg tagcagcacc cacggagaga tgtgagcaag 780
ccgctttgat gtaaaatgtc ggtatagatt ctcgagacca catccggtgc aaaactggca 840
ccattatctc cacctagagt tttgtactgt agagatcatg acattttata gtaacttcag 900
attcatcgaa ataaaaatagg gggttctctg caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 960
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
aaaaaaaaaa aa 1032

<210> 32
<211> 263
<212> PRT
<213> Triticum aestivum

<400> 32
Thr Arg Asp Ala Val Leu Glu Ala Ala Lys Lys Ala Lys Glu Ala Gly
1 5 10 15

Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg Glu Thr Ile Gly Arg
 20 25 30
 Lys Thr Asn Phe Asn Gln Ile Leu Glu Tyr Val Lys Asp Ile Arg Gly
 35 40 45
 Met Gly Met Glu Val Cys Cys Thr Leu Gly Met Leu Glu Lys Gln Gln
 50 55 60
 Ala Glu Glu Leu Lys Lys Ala Gly Leu Thr Ala Tyr Asn His Asn Leu
 65 70 75 80
 Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Ile Ile Ser Thr Arg Ser Tyr
 85 90 95
 Asp Asp Arg Leu Gln Thr Leu Gln His Val Arg Glu Ala Gly Ile Ser
 100 105 110
 Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu Ala Glu Glu Asp Arg
 115 120 125
 Val Gly Leu Leu His Thr Leu Ala Thr Leu Pro Thr His Pro Glu Ser
 130 135 140
 Val Pro Ile Asn Ala Leu Ile Ala Val Lys Gly Thr Pro Leu Gln Asp
 145 150 155 160
 Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg Met Ile Ala Ser Ala
 165 170 175
 Arg Ile Val Met Pro Lys Ala Met Val Arg Leu Ser Ala Gly Arg Val
 180 185 190
 Arg Phe Ser Met Pro Glu Gln Ala Leu Cys Phe Leu Ala Gly Ala Asn
 195 200 205
 Ser Ile Phe Ala Gly Glu Lys Leu Leu Thr Thr Ala Asn Asn Asp Phe
 210 215 220
 Asp Ala Asp Gln Ala Met Phe Lys Ile Leu Gly Leu Ile Pro Lys Ala
 225 230 235 240
 Pro Asn Phe Gly Asp Glu Glu Val Met Val Ala Ala Pro Thr Glu Arg
 245 250 255
 Cys Glu Gln Ala Ala Leu Met
 260

<210> 33
 <211> 378
 <212> PRT
 <213> Arabidopsis thaliana

<400> 33
 Met Met Leu Val Arg Ser Val Phe Arg Ser Gln Leu Arg Pro Ser Val
 1 5 10 15
 Ser Gly Gly Leu Gln Ser Ala Ser Cys Tyr Ser Ser Leu Ser Ala Ala
 20 25 30
 Ser Ala Glu Ala Glu Arg Thr Ile Arg Glu Gly Pro Arg Asn Asp Trp
 35 40 45
 Ser Arg Asp Glu Ile Lys Ser Val Tyr Asp Ser Pro Leu Leu Asp Leu
 50 55 60
 Leu Phe His Gly Ala Gln Val His Arg His Val His Asn Phe Arg Glu
 65 70 75 80
 Val Gln Gln Cys Thr Leu Leu Ser Ile Lys Thr Gly Gly Cys Ser Glu
 85 90 95
 Asp Cys Ser Tyr Cys Pro Gln Ser Ser Arg Tyr Ser Thr Gly Val Lys
 100 105 110
 Ala Gln Arg Leu Met Ser Lys Asp Ala Val Ile Asp Ala Ala Lys Lys
 115 120 125

Ala Lys Glu Ala Gly Ser Thr Arg Phe Cys Met Gly Ala Ala Trp Arg
130 135 140
Asp Thr Ile Gly Arg Lys Thr Asn Phe Ser Gln Ile Leu Glu Tyr Ile
145 150 155 160
Lys Glu Ile Arg Gly Met Gly Met Glu Val Cys Cys Thr Leu Gly Met
165 170 175
Ile Glu Lys Gln Gln Ala Leu Glu Leu Lys Lys Ala Gly Leu Thr Ala
180 185 190
Tyr Asn His Asn Leu Asp Thr Ser Arg Glu Tyr Tyr Pro Asn Val Ile
195 200 205
Thr Thr Arg Ser Tyr Asp Asp Arg Leu Glu Thr Leu Ser His Val Arg
210 215 220
Asp Ala Gly Ile Asn Val Cys Ser Gly Gly Ile Ile Gly Leu Gly Glu
225 230 235 240
Ala Glu Glu Asp Arg Ile Gly Leu Leu His Thr Leu Ala Thr Leu Pro
245 250 255
Ser His Pro Glu Ser Val Pro Ile Asn Ala Leu Leu Ala Val Lys Gly
260 265 270
Thr Pro Leu Glu Asp Gln Lys Pro Val Glu Ile Trp Glu Met Ile Arg
275 280 285
Met Ile Gly Thr Ala Arg Ile Val Met Pro Lys Ala Met Val Arg Leu
290 295 300
Ser Ala Gly Arg Val Arg Phe Ser Met Ser Glu Gln Ala Leu Cys Phe
305 310 315 320
Leu Ala Gly Ala Asn Ser Ile Phe Thr Gly Glu Lys Leu Leu Thr Thr
325 330 335
Pro Asn Asn Asp Phe Asp Ala Asp Gln Leu Met Phe Lys Thr Leu Gly
340 345 350
Leu Ile Pro Lys Pro Pro Ser Phe Ser Glu Asp Asp Ser Glu Ser Glu
355 360 365
Asn Cys Glu Lys Val Ala Ser Ala Ser His
370 375

<210> 34
<211> 362
<212> PRT
<213> Saccharomyces cerevisiae

<400> 34
Met Phe Thr Arg Thr Ile Arg Gln Gln Ile Arg Arg Phe Phe Ala Leu
1 5 10 15
Phe Leu Val Arg Asn Asn Trp Thr Arg Glu Glu Ile Gln Lys Ile Tyr
20 25 30
Asp Thr Pro Leu Ile Asp Leu Ile Phe Arg Ala Ala Ser Ile His Arg
35 40 45
Lys Phe His Asp Pro Lys Lys Val Gln Gln Cys Thr Leu Leu Ser Ile
50 55 60
Lys Thr Gly Gly Cys Thr Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser
65 70 75 80
Arg Tyr Asn Thr Gly Val Lys Ala Thr Lys Leu Met Lys Ile Asp Glu
85 90 95
Val Leu Glu Lys Ala Lys Ile Ala Lys Ala Lys Gly Ser Thr Arg Phe
100 105 110
Cys Met Gly Ser Ala Trp Arg Asp Leu Asn Gly Arg Asn Arg Thr Phe
115 120 125

Lys Asn Ile Leu Glu Ile Ile Lys Glu Val Arg Ser Met Asp Met Glu
130 135 140
Val Cys Val Thr Leu Gly Met Leu Asn Glu Gln Gln Ala Lys Glu Leu
145 150 155 160
Lys Asp Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg
165 170 175
Glu Tyr Tyr Ser Lys Ile Ile Ser Thr Arg Thr Tyr Asp Glu Arg Leu
180 185 190
Asn Thr Ile Asp Asn Leu Arg Lys Ala Gly Leu Lys Val Cys Ser Gly
195 200 205
Gly Ile Leu Gly Leu Gly Glu Lys Lys His Asp Arg Val Gly Leu Ile
210 215 220
His Ser Leu Ala Thr Met Pro Thr His Pro Glu Ser Val Pro Phe Asn
225 230 235 240
Leu Leu Val Pro Ile Pro Gly Thr Pro Val Gly Asp Ala Val Lys Glu
245 250 255
Arg Leu Pro Ile His Pro Phe Leu Arg Ser Ile Ala Thr Ala Arg Ile
260 265 270
Cys Met Pro Lys Thr Ile Ile Arg Phe Ala Ala Gly Arg Asn Thr Cys
275 280 285
Ser Glu Ser Glu Gln Ala Leu Ala Phe Met Ala Gly Ala Asn Ala Val
290 295 300
Phe Thr Gly Glu Lys Met Leu Leu Leu Leu Phe Leu Asp Ser Asp
305 310 315 320
Ser Gln Leu Phe Tyr Asn Trp Gly Leu Glu Gly Met Gln Ser Phe Glu
325 330 335
Tyr Gly Thr Ser Thr Glu Gly Glu Asp Gly Thr Phe Thr Leu Pro Pro
340 345 350
Lys Glu Arg Leu Ala Pro Ser Pro Ser Leu
355 360

<210> 35
<211> 363
<212> PRT
<213> Schizosaccharomyces pombe

<400> 35
Met Phe Thr Arg Thr Ile Arg Gln Gln Ile Arg Arg Ser Ser Ala Leu
1 5 10 15
Ser Leu Val Arg Asn Asn Trp Thr Arg Glu Glu Ile Gln Lys Ile Tyr
20 25 30
Asp Thr Pro Leu Ile Asp Leu Ile Phe Arg Ala Ala Ser Ile His Arg
35 40 45
Lys Phe His Asp Pro Lys Lys Val Gln Gln Cys Thr Leu Leu Ser Ile
50 55 60
Lys Thr Gly Gly Cys Thr Glu Asp Cys Lys Tyr Cys Ala Gln Ser Ser
65 70 75 80
Arg Tyr Asn Thr Gly Val Lys Ala Thr Lys Leu Met Lys Ile Asp Glu
85 90 95
Val Leu Glu Lys Ala Lys Ile Ala Lys Ala Lys Gly Ser Thr Arg Phe
100 105 110
Cys Met Gly Ser Ala Trp Arg Asp Leu Asn Gly Arg Asn Arg Thr Phe
115 120 125
Lys Asn Ile Leu Glu Ile Ile Lys Glu Val Arg Ser Met Asp Met Glu
130 135 140

Val Cys Val Thr Leu Gly Met Leu Asn Glu Gln Gln Ala Lys Glu Leu
 145 150 155 160
 Lys Asp Ala Gly Leu Thr Ala Tyr Asn His Asn Leu Asp Thr Ser Arg
 165 170 175
 Glu Tyr Tyr Ser Lys Ile Ile Ser Thr Arg Thr Tyr Asp Glu Arg Leu
 180 185 190
 Asn Thr Ile Asp Asn Leu Arg Lys Ala Gly Leu Lys Val Cys Ser Gly
 195 200 205
 Gly Ile Leu Gly Leu Gly Glu Lys Lys His Asp Arg Val Gly Leu Ile
 210 215 220
 His Ser Leu Ala Thr Met Pro Thr His Pro Glu Ser Val Pro Phe Asn
 225 230 235 240
 Leu Leu Val Pro Ile Pro Gly Thr Pro Val Gly Asp Ala Val Lys Glu
 245 250 255
 Arg Leu Pro Ile His Pro Phe Leu Arg Ser Ile Ala Thr Ala Arg Ile
 260 265 270
 Cys Met Pro Lys Thr Ile Ile Arg Phe Ala Ala Gly Arg Asn Thr Cys
 275 280 285
 Ser Glu Ser Glu Gln Ala Leu Ala Phe Met Ala Gly Ala Asn Ala Val
 290 295 300
 Phe Thr Gly Glu Lys Met Leu Thr Thr Pro Ala Val Ser Trp Asp Ser
 305 310 315 320
 Asp Ser Gln Leu Phe Tyr Asn Trp Gly Leu Glu Gly Met Gln Ser Phe
 325 330 335
 Glu Tyr Gly Thr Ser Thr Glu Gly Glu Asp Gly Thr Phe Thr Leu Pro
 340 345 350
 Pro Lys Glu Arg Leu Ala Pro Ser Pro Ser Leu
 355 360

<210> 36
 <211> 12
 <212> PRT
 <213> biotin synthase conserved sequence element

<220>
 <221> UNSURE
 <222> (2)..(2)
 <223> Xaa represents any amino acid

<220>
 <221> UNSURE
 <222> (4)..(4)
 <223> Xaa represents any amino acid

<220>
 <221> UNSURE
 <222> (8)..(8)
 <223> Xaa represents any amino acid

<220>
 <221> UNSURE
 <222> (11)..(11)



223> Xaa represents any amino acid

<400> 36

Gly Xaa Cys Xaa Glu Asp Cys Xaa Tyr Cys Xaa Gln
1 5 10